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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=18; min=57; sec=29; ms=694;
]

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Reviewer Comments:

<210> 25

<211> 189

<212> DNA

<213> Synthetic intron

<400> 25

<210> 29

<211> 20

<212> PRT

<213> Synthetic

The above <213> responses for sequence id#'s 25 and 29 are both
invalid, please correct the remaining sequences showing similar errors.

Application No: 10596010 Version No: 2.0

Input Set:**Output Set:**

Started: 2008-10-21 11:04:20.060
Finished: 2008-10-21 11:04:21.978
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 918 ms
Total Warnings: 16
Total Errors: 2
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
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W 402	Undefined organism found in <213> in SEQ ID (26)
E 356	Organism is not permitted in <213> in SEQ ID (29)
E 356	Organism is not permitted in <213> in SEQ ID (30)

SEQUENCE LISTING

<110> Copenhagen University Tech Trans Enheden
 Andreasson, Erik
 Jenkins, Tom
 Mundy, John
 Petersen, Nikolaj H.T.
 Brodersen, Peter
 Thorgrimsen, Stefan
 Rocher, Anne

<120> Plant Disease Resistance and SAR Regulator Protein

<130> 09663.0068USWO

<140> 10596010
 <141> 2008-10-21

<150> PCT/DK2004/000822
 <151> 2004-11-26

<150> DK PA200301759
 <151> 2003-11-28

<150> US 60/526,319
 <151> 2003-12-01

<160> 30

<170> PatentIn version 3.5

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aac cag aag cgg cag ctt cag atc tgt ggt cct cgt cct tca cct ctt 96
 Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
 20 25 30

agt gtt cac aaa gac tct cac aaa atc aag aaa cct cca aaa cac cct 144
 Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
 35 40 45

gcg ccg ccg cca aat cgt gac caa ccg ccg ccg tat att cct aga gag 192
 Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu

50	55	60	
ccg gtg gtt atc tac gcc gta tcc ccc aag gtt gta cac gca acc gcg			240
Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala			
65	70	75	80
tct gag ttc atg aac gta gtc cag cga ctc aca ggg atc tcc tct ggt			288
Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly			
	85	90	95
gtt ttc ctc gaa tct ggc ggc ggt gga gat gtt tca ccg gcg gcg agg			336
Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg			
	100	105	110
cta gcg tcc acg gaa aat gct agt cca aga gga gga aaa gaa ccg gct			384
Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala			
	115	120	125
gcg aga gat gag acg gtg gaa atc aac acg gct atg gaa gaa gca gct			432
Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala			
	130	135	140
gaa ttt ggt ggt tat gct ccg gga ata ctc tcg cca tct ccg gcc ttg			480
Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu			
145	150	155	160
ttg cca aca gct tct acc ggg ata ttc tct ccg atg tat cat caa ggt			528
Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly			
	165	170	175
ggg atg ttt tcg ccg gct ata cca ctg gga tta ttc tcg ccg gcg gga			576
Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly			
	180	185	190
ttt atg agc ccg ttt cga agt cct ggc ttt act agt ttg gta gct tca			624
Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser			
	195	200	205
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 <212> PRT
 <213> Arabidopsis sp.

<400> 2

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5
10
15

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20
25
30

Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
 35 40 45

Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu
 50 55 60

Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala
 65 70 75 80

Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly
 85 90 95

Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg
 100 105 110

Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala
 115 120 125

Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala
 130 135 140

Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu
 145 150 155 160

Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly
 165 170 175

Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly
 180 185 190

Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser
 195 200 205

Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp
 210 215 220

<210> 3
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 <213> Arabidopsis sp.

<400> 3
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 <222> (1)..(720)

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 ata cca ttg aaa gtc cgt gga gat tcg cac aag atc atc aag aag cca 96
 Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro
 20 25 30

 cca cta gcg ccg cca cac ccg caa cca caa cca cca caa acc cat cag 144
 Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln
 35 40 45

 caa gaa ccg tca caa tcg cgg ccg cca cct ggt ccc gtg att ata tac 192
 Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr
 50 55 60

 aca gta tct ccc agg att atc cat aca cac cct aat aac ttc atg aca 240
 Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr
 65 70 75 80

 ttg gtc caa cgt ctc aca ggt aaa acc tcc acc tcc aca aca tcc tcc 288
 Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser
 85 90 95

 tcc tat tct tca tct acg tca gca cca aaa gac gcg tca aca atg gtt 336
 Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val
 100 105 110

 gat aca tct cat ggg ttg ata tct ccg gcg gct cgg ttt gct gtt aca 384
 Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
 115 120 125

 gag aag gct aat atc tca aac gaa cta ggg aca ttt gtt gga ggc gaa 432
 Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu
 130 135 140

ggg act atg gat caa tat tat cat tat cat cat cat cat cat cat caa	480
Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His His Gln	
145 150 155 160	
gaa caa caa cat caa aat caa ggg ttc gag cgg cca agt ttc cac cat	528
Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His	
165 170 175	
gct ggg att tta tcg ccg gga cct aat tct ctg ccg tcg gta tca ccg	576
Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro	
180 185 190	
gac ttc ttt tcc act att gga cca acc gat cca caa ggt ttt tcg tcg	624
Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser	
195 200 205	
ttc ttt aat gac ttt aac tct atc ctt cag agt agt cca tcg aag att	672
Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile	
210 215 220	
cag tct cct tct tct atg gac ctt ttc aac aat ttc ttt gat tct tga	720
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225 230 235	
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35 40 45	
Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr	
50 55 60	
Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr	
65 70 75 80	
Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser	
85 90 95	
Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val	

100

105

110

Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
 115 120 125

Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu
 130 135 140

Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His His Gln
 145 150 155 160

Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His
 165 170 175

Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro
 180 185 190

Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser
 195 200 205

Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile
 210 215 220

Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser
 225 230 235

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<212> DNA

<213> Arabidopsis sp.

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<210> 8

<211> 21

<212> DNA

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<400> 8

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21

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<213> Brassica oleracea

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<222> (139)..(789)

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aactcttttg agaaaata atg gat ccg tcg gag tct ttc gcc ggc ggc aat 171
Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn
1 5 10

cct tcc gac caa cag aac cag aaa cgt cag ctt cag atc tgt ggt cct 219
Pro Ser Asp Gln Gln Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro
15 20 25

cgt ccc tca cct ctc agc gtc aac aaa gac tct cac aag atc aag aaa 267
Arg Pro Ser Pro Leu Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys
30 35 40

cct cct aaa cac cct gct cct ccg cct cag cat cgc gac caa gct ccg 315
Pro Pro Lys His Pro Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro
45 50 55

ctc tac gct gct cga gag ccg gtg gtc atc tac gcc gtc tcg ccg aaa 363
Leu Tyr Ala Ala Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys
60 65 70 75

gtc gtc cac acc aca gcc tcg gat ttc atg aac gtc gtc cag cgt ctc 411
Val Val His Thr Thr Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu
80 85 90

acc ggc atc tca tcc gcc gtc ttc ctc gaa tcc ggt aac ggc gga gat 459
Thr Gly Ile Ser Ser Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp
95 100 105

gta tct ccg gcg gcg aga ctc gcc gcg acc gag aat gca agc ccg aga 507
Val Ser Pro Ala Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg
110 115 120

gga gga aaa gaa ccg gtg atg gcg gct aaa gat gag acg gtg gaa atc 555
Gly Gly Lys Glu Pro Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile
125 130 135

gcg acg gct atg gaa gaa gca gcc gag ttg agc ggc tat gcg ccg ggg 603
Ala Thr Ala Met Glu Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly
140 145 150 155

ata ctc tcc cct tct ccg gct atg tta ccg aca gct tct gcc gga ata 651
Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile
160 165 170

ttc tcg cag atg act act cac caa ggt ggg atg ttc tcg ccg gga ttg 699
Phe Ser Gln Met Thr Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu

175	180	185	
ttt tgc ccg gcg ggg tta atg agc ccg ttt ggt ttt gct agc ttg gtt			747
Phe Ser Pro Ala Gly Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val			
190	195	200	
gct tct cca acg ttt gct gat ttg ttc agt cat att tgg gga ta			791
Ala Ser Pro Thr Phe Ala Asp Leu Phe Ser His Ile Trp Gly			
205	210	215	
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Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro			
35	40	45	
Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg			
50	55	60	
Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr			
65	70	75	80
Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser			
85	90	95	
Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp Val Ser Pro Ala Ala			
100	105	110	
Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro			
115	120	125	
Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu			
130	135	140	
Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser			
145	150	155	160

Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr
165 170 175

Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly
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<222> (198)..(833)

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